RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/764,730
Source: TWO
Date Processed by STIC: 10/20/04

ENTERED

IFWO

RAW SEQUENCE LISTING   DATE: 10/20/2004
PATENT APPLICATION: **US/10/764,730**   TIME: 16:45:49

Input Set : **A:\Seqlist.txt**
Output Set: **N:\CRF4\10202004\J764730.raw**

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 4 <110> APPLICANT: Mueller-Hermelink, Hans Konrad
 5        Vollmers, Heinz Peter
 6        Hensel, Frank
 8 <120> TITLE OF INVENTION: Neoplasm-Specific Polypeptides and Their
 9        Uses
11 <130> FILE REFERENCE: 50308/009002
13 <140> CURRENT APPLICATION NUMBER: 10/764,730
14 <141> CURRENT FILING DATE: 2004-01-26
16 <150> PRIOR APPLICATION NUMBER: PCT/DE02/02699
17 <151> PRIOR FILING DATE: 2002-07-23
19 <150> PRIOR APPLICATION NUMBER: DE 10210425.5
20 <151> PRIOR FILING DATE: 2002-03-09
22 <150> PRIOR APPLICATION NUMBER: DE 10136009.6
23 <151> PRIOR FILING DATE: 2001-07-24
25 <160> NUMBER OF SEQ ID NOS: 30
27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 288
31 <212> TYPE: DNA
32 <213> ORGANISM: Mus musculus
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (1)...(288)
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40 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile Asn Trp
41 1               5                   10                  15
43 gtg aag cag agg act gga cag ggc ctt gag tgg att gga gag att tat     96
44 Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr
45             20                  25                  30
47 cct gga agt ggt aat act tac tac aat gag aag ttc aag ggc aag gcc    144
48 Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala
49             35                  40                  45
51 aca ctg act gca gac aaa tcc tcc agc aca gcc tac atg cag ctc agc    192
52 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
53         50                  55                  60
55 agc ctg aca tct gag gac tct gca gtc tat ttc tgt gca aga tcg gga    240
56 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Ser Gly
57 65                  70                  75                  80
59 tta cga ccc tat gct atg gac tac tgg ggt caa gga acc tca gtc acc    288
60 Leu Arg Pro Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
61             85                  90                  95
65 <210> SEQ ID NO: 2
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66 <211> LENGTH: 96
67 <212> TYPE: PRT
68 <213> ORGANISM: Mus musculus
70 <400> SEQUENCE: 2
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72 1               5                   10                  15
73 Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr
74              20                  25                  30
75 Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala
76          35                  40                  45
77 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
78     50                  55                  60
79 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Ser Gly
80 65                  70                  75                  80
81 Leu Arg Pro Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
82              85                  90                  95
85 <210> SEQ ID NO: 3
86 <211> LENGTH: 315
87 <212> TYPE: DNA
88 <213> ORGANISM: Mus musculus
90 <220> FEATURE:
91 <221> NAME/KEY: CDS
92 <222> LOCATION: (1)...(315)
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96 Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
97 1               5                   10                  15
99 aga tct agt cag agc att gta cat agt aat gga aac acc tat tta gaa   96
100 Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
101             20                  25                  30
103 tgg tac ctg cag aaa cca ggc cag tct cca aag ctc ctg atc tac aaa  144
104 Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
105             35                  40                  45
107 gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga  192
108 Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
109     50                  55                  60
111 tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat  240
112 Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
113 65                  70                  75                  80
115 ctg gga gtt tat tac tgc ttt caa ggt tca cat gtt ccg tac acg ttc  288
116 Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe
117             85                  90                  95
119 gga ggg ggg acc aag ctg gaa ata aaa                              315
120 Gly Gly Gly Thr Lys Leu Glu Ile Lys
121             100                 105
124 <210> SEQ ID NO: 4
125 <211> LENGTH: 105
126 <212> TYPE: PRT
127 <213> ORGANISM: Mus musculus
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129 <400> SEQUENCE: 4
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132 Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
133             20                  25                  30
134 Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
135         35                  40                  45
136 Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
137     50                  55                  60
138 Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
139 65                  70                  75                  80
140 Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe
141             85                  90                  95
142 Gly Gly Gly Thr Lys Leu Glu Ile Lys
143             100                 105

146 <210> SEQ ID NO: 5
147 <211> LENGTH: 3114
148 <212> TYPE: DNA
149 <213> ORGANISM: Homo sapiens
151 <220> FEATURE:
152 <221> NAME/KEY: CDS
153 <222> LOCATION: (1)...(3114)
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157 Asp Val Arg Glu Pro Glu Asn Glu Ile Ser Ser Asp Cys Asn His Leu
158 1               5                   10                  15  .
160 ttg tgg aat tat aag ctg aac cta act aca gat ccc aaa ttt gaa tct      96
161 Leu Trp Asn Tyr Lys Leu Asn Leu Thr Thr Asp Pro Lys Phe Glu Ser
162             20                  25                  30
164 gtg gcc aga gag gtt tgc aaa tct act ata aca gag att gaa gaa tgt     144
165 Val Ala Arg Glu Val Cys Lys Ser Thr Ile Thr Glu Ile Glu Glu Cys
166             35                  40                  45
168 gct gat gaa ccg gtt gga aaa ggt tac atg gtt tcc tgc ttg gtg gat     192
169 Ala Asp Glu Pro Val Gly Lys Gly Tyr Met Val Ser Cys Leu Val Asp
170     50                  55                  60
172 cac cga ggc aac atc act gag tat cag tgt cac cag tac att acc aag     240
173 His Arg Gly Asn Ile Thr Glu Tyr Gln Cys His Gln Tyr Ile Thr Lys
174 65                  70                  75                  80
176 atg acg gcc atc att ttt agt gat tac cgt tta atc tgt ggc ttc atg     288
177 Met Thr Ala Ile Ile Phe Ser Asp Tyr Arg Leu Ile Cys Gly Phe Met
178             85                  90                  95
180 gat gac tgc aaa aat gac atc aac att ctg aaa tgt ggc agt att cgg     336
181 Asp Asp Cys Lys Asn Asp Ile Asn Ile Leu Lys Cys Gly Ser Ile Arg
182             100                 105                 110
184 ctt gga gaa aag gat gca cat tca caa ggt gag gtg gta tca tgc ttg     384
185 Leu Gly Glu Lys Asp Ala His Ser Gln Gly Glu Val Val Ser Cys Leu
186             115                 120                 125
188 gag aaa ggc ctg gtg aaa gaa gca gaa gaa aga gaa ccc aag att caa     432
189 Glu Lys Gly Leu Val Lys Glu Ala Glu Glu Arg Glu Pro Lys Ile Gln
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190     130                   135                   140
192 gtt tct gaa ctc tgc aag aaa gcc att ctc cgg gtg gct gag ctg tca    480
193 Val Ser Glu Leu Cys Lys Lys Ala Ile Leu Arg Val Ala Glu Leu Ser
194 145                   150                   155                   160
196 tcg gat gac ttt cac tta gac cgg cat tta tat ttt gct tgc cga gat    528
197 Ser Asp Asp Phe His Leu Asp Arg His Leu Tyr Phe Ala Cys Arg Asp
198                   165                   170                   175
200 gat cgg gag cgt ttt tgt gaa aat aca caa gct ggt gag ggc aga gtg    576
201 Asp Arg Glu Arg Phe Cys Glu Asn Thr Gln Ala Gly Glu Gly Arg Val
202                   180                   185                   190
204 tat aag tgc ctc ttt aac cat aaa ttt gaa gaa tcc atg agt gaa aag    624
205 Tyr Lys Cys Leu Phe Asn His Lys Phe Glu Glu Ser Met Ser Glu Lys
206             195                   200                   205
208 tgt cga gaa gca ctt aca acc cgc caa aag ctg att gcc cag gat tat    672
209 Cys Arg Glu Ala Leu Thr Thr Arg Gln Lys Leu Ile Ala Gln Asp Tyr
210     210                   215                   220
212 aaa gtc agt tat tca ttg gcc aaa tcc tgt aaa agt gac ttg aag aaa    720
213 Lys Val Ser Tyr Ser Leu Ala Lys Ser Cys Lys Ser Asp Leu Lys Lys
214 225                   230                   235                   240
216 tac cgg tgc aat gtg gaa aac ctt ccg cga tcg cgt gaa gcc agg ctc    768
217 Tyr Arg Cys Asn Val Glu Asn Leu Pro Arg Ser Arg Glu Ala Arg Leu
218                   245                   250                   255
220 tcc tac ttg tta atg tgc ctg gag tca gct gta cac aga ggg cga caa    816
221 Ser Tyr Leu Leu Met Cys Leu Glu Ser Ala Val His Arg Gly Arg Gln
222             260                   265                   270
224 gtc agc agt gag tgc cag ggg gag atg ctg gat tac cga cgc atg ttg    864
225 Val Ser Ser Glu Cys Gln Gly Glu Met Leu Asp Tyr Arg Arg Met Leu
226             275                   280                   285
228 atg gaa gac ttt tct ctg agc cct gag atc atc cta agc tgt cgg ggg    912
229 Met Glu Asp Phe Ser Leu Ser Pro Glu Ile Ile Leu Ser Cys Arg Gly
230     290                   295                   300
232 gag att gaa cac cat tgt tcc gga tta cat cga aaa ggg cgg acc cta    960
233 Glu Ile Glu His His Cys Ser Gly Leu His Arg Lys Gly Arg Thr Leu
234 305                   310                   315                   320
236 cac tgt ctg atg aaa gta gtt cga ggg gag aag ggg aac ctt gga atg    1008
237 His Cys Leu Met Lys Val Val Arg Gly Glu Lys Gly Asn Leu Gly Met
238             325                   330                   335
240 aac tgc cag cag gcg ctt caa aca ctg att cag gag act gac cct ggt    1056
241 Asn Cys Gln Gln Ala Leu Gln Thr Leu Ile Gln Glu Thr Asp Pro Gly
242             340                   345                   350
244 gca gat tac cgc att gat cga gct ttg aat gaa gct tgt gaa tct gta    1104
245 Ala Asp Tyr Arg Ile Asp Arg Ala Leu Asn Glu Ala Cys Glu Ser Val
246             355                   360                   365
248 atc cag aca gcc tgc aaa cat ata aga tct gga gac cca atg atc ttg    1152
249 Ile Gln Thr Ala Cys Lys His Ile Arg Ser Gly Asp Pro Met Ile Leu
250     370                   375                   380
252 tcg tgc ctg atg gaa cat tta tac aca gag aag atg gta gaa gac tgt    1200
253 Ser Cys Leu Met Glu His Leu Tyr Thr Glu Lys Met Val Glu Asp Cys
254 385                   390                   395                   400
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256 gaa cac cgt ctc tta gag ctg cag tat ttc atc tcc cgg gat tgg aag   1248
257 Glu His Arg Leu Leu Glu Leu Gln Tyr Phe Ile Ser Arg Asp Trp Lys
258             405                 410                 415
260 ctg gac cct gtc ctg tac cgc aag tgc cag gga gac gct tct cgt ctt   1296
261 Leu Asp Pro Val Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu
262             420                 425                 430
264 tgc cac acc cac ggt tgg aat gag acc agc gaa ttt atg cct cag gga   1344
265 Cys His Thr His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly
266             435                 440                 445
268 gct gtg ttc tct tgt tta tac aga cac gcc tac cgc act gag gaa cag   1392
269 Ala Val Phe Ser Cys Leu Tyr Arg His Ala Tyr Arg Thr Glu Glu Gln
270         450                 455                 460
272 gga agg agg ctc tca cgg gag tgc cga gct gaa gtc caa agg atc cta   1440
273 Gly Arg Arg Leu Ser Arg Glu Cys Arg Ala Glu Val Gln Arg Ile Leu
274 465                 470                 475                 480
276 cac cag cgt gcc atg gat gtc aag ctg gat cct gcc ctc cag gat aag   1488
277 His Gln Arg Ala Met Asp Val Lys Leu Asp Pro Ala Leu Gln Asp Lys
278                 485                 490                 495
280 tgc ctg att gat ctg gga aaa tgg tgc agt gag aaa aca gag act gga   1536
281 Cys Leu Ile Asp Leu Gly Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly
282             500                 505                 510  .
284 cag aag ctg gag tgc ctt cag gac cat ctg gat gac tta gtg gtg gag   1584
285 Gln Lys Leu Glu Cys Leu Gln Asp His Leu Asp Asp Leu Val Val Glu
286             515                 520                 525
288 tgt aga gat ata gtt ggc aac ctc act gag tta gaa tca gag gat att   1632
289 Cys Arg Asp Ile Val Gly Asn Leu Thr Glu Leu Glu Ser Glu Asp Ile
290         530                 535                 540
292 caa ata gaa gcc ttg ctg atg aga gcc tgt gag ccc ata att cag aac   1680
293 Gln Ile Glu Ala Leu Leu Met Arg Ala Cys Glu Pro Ile Ile Gln Asn
294 545                 550                 555                 560
296 ttc tgc cac gat gtg gca gat aac cag ata gac tcc ggg gac ctg atg   1728
297 Phe Cys His Asp Val Ala Asp Asn Gln Ile Asp Ser Gly Asp Leu Met
298                 565                 570                 575
300 gag tgt ctg ata cag aac aaa cac cag aag gac atg aac gag aag tgt   1776
301 Glu Cys Leu Ile Gln Asn Lys His Gln Lys Asp Met Asn Glu Lys Cys
302             580                 585                 590
304 gcc atc gga gtt acc cac ttc cag ctg gtg cag atg aag gat ttt cgg   1824
305 Ala Ile Gly Val Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg
306             595                 600                 605
308 ttt tct tac aag ttt aaa atg gcc tgc aag gag gac gtg ttg aag ctt   1872
309 Phe Ser Tyr Lys Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu
310         610                 615                 620
312 tgc cca aac ata aaa aag aag gtg gac gtg gtg atc tgc ctg agc acg   1920
313 Cys Pro Asn Ile Lys Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr
314 625                 630                 635                 640
316 acc gtg cgc aat gac act ctg cag gaa gcc aag gag cac agg gtg tcc   1968
317 Thr Val Arg Asn Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser
318             645                 650                 655
320 ctg aag tgc cgc agg cag ctc cgt gtg gag gag ctg gag atg acg gag   2016
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/764,730**

DATE: 10/20/2004
TIME: 16:45:50

Input Set : **A:\Seqlist.txt**
Output Set: **N:\CRF4\10202004\J764730.raw**

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L:1105 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:1103